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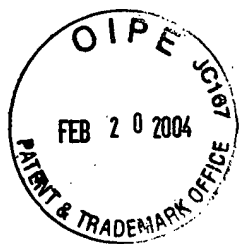
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Replacement Sheet

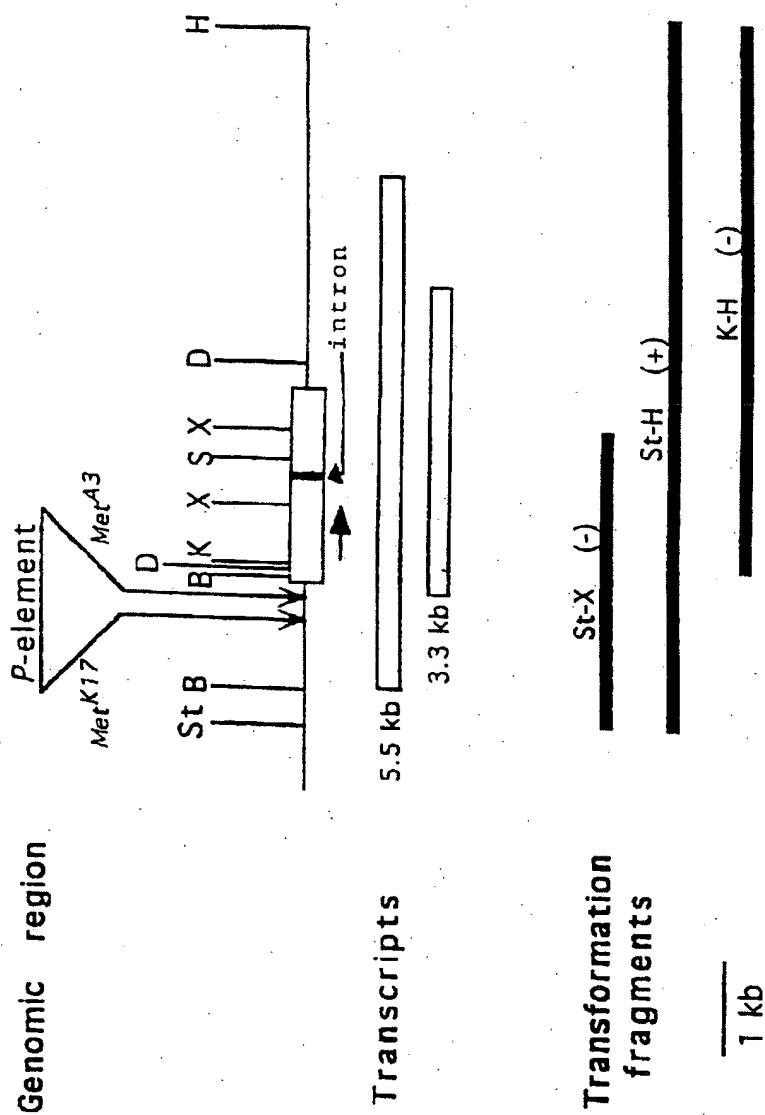


FIGURE 1

Replacement Sheet

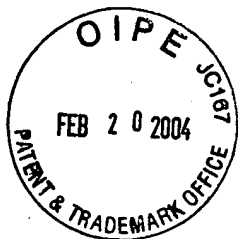
6.2341dbGENOMICS

[illegible]

FIGURE 2



FIGURE 3B



Replacement Sheet

1 MAAPETGNTGSTGSAGSTGSGSGSGSGSGSSSDPANGREA AA Genomic
1 MAAPETGNTGSTGSAGSTGSGSGSGSGSGSSSDPANGREA cDNA

41 RNLA EKQRRDKLN ASI QELATMVPHAAESSRRLDKTAVLR AA Genomic
41 RNLA EKQRRDKLN ASI QELATMVPHAAESSRRLDKTAVLR cDNA

81 FATHGLRLQYVFGKSASRRRKKTGLKGTGMSASPVGDLPN AA Genomic
81 FATHGLRLQYVFGKSASRRRKKTGLKGTGMSASPVGDLPN cDNA

121 PSLHLTDTLMQLLDCCFLTTLTCSGQIVLVSTSV EQLLGHC AA Genomic
121 PSLHLTDTLMQLLDCCFLTTLTCSGQIVLVSTSV EQLLGHC cDNA

161 QSDLYGQNL LQITHPDDQDLLRQQLIPRDIETLFYQH QHH AA Genomic
161 QSDLYGQNL LQITHPDDQDLLRQQLIPRDIETLFYQH QHH cDNA

201 QQQGHNPQQHSTSTSA S XSGSDLEEEEMETEEHRLGRQQG AA Genomic
201 QQQGHNPQQHSTSTSA S A SGSDLEEEEMETEEHRLGRQQG cDNA

241 EADDDDEDHPYNRRTPSPRRMAHLATIDDRLRMDRRRCFTVR AA Genomic
241 EADDDDEDHPYNRRTPSPRRMAHLATIDDRLRMDRCFTVR cDNA

281 LARASTRAEATRHYERVKIDGCFRRSDSSLTGGAAANYPI AA Genomic
281 LARASTRAEATRHYERVKIDGCFRRSDSSLTGGAAANYPI cDNA

321 VSQ LIRRSRNNNMLAAAAA VAAEAATVPPQHDAIAQAALH AA Genomic
321 VSQ LIRRSRNNNMLAAAAA VAAEAATVPPQHDAIAQAALH cDNA

361 GISGNDIVLVAMARVLR EERPPETEETGTVGLTIYRQPEPY AA Genomic
361 GISGNDIVLVAMARVLR EERPPETEETGTVGLTIYRQPEPY cDNA

401 QLEYHTRHLIDGSIIDCDQRI GLVAGYMKDEV GILTSSL AA Genomic
401 QLEYHTRHLIDGSIIDCDQRI GLVAGYMKDEV cDNA

441 TAYDN SCTLH SKQVRNLSPFCFMHLDDVRWVIVALRQMY AA Genomic
433 RNLSPFCFMHLDDVRWVIVALRQMY cDNA

481 DCNSDYGESCYRLLSRNGRFIYLHTKGFLEVDRGSNKVHS AA Genomic
458 DCNSDYGESCYRLLSRNGRFIYLHTKGFLEVDRGSNKVHS cDNA

521 FLCVNTLLDEEAGRQKVQENKEKFSTIIKAEMPTQSSSPD AA Genomic
498 FLCVNTLLDEEAGRQKVQENKEKFSTIIKAEMPTQSSSPD cDNA

561 LPASQAPQQLERIVLYLIENLQKSVDSAETVGGQGME SLM AA Genomic
538 LPASQAPQQLERIVLYLIENLQKSVDSAETVGGQGME SLM cDNA

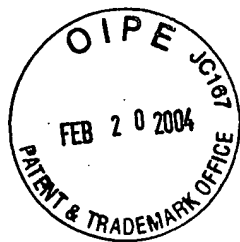
601 DDGYSSPANTLTLEELAPSPTPALALVPPAPSSSVKSSISK AA Genomic
578 DDGYSSPANTLTLEELAPSPTPALALVPPAPSSSVKSSISK cDNA

641 SVSVVNVTAARKFQQEHQKQRE RDREQLKERTNSTQG VIR AA Genomic
618 SVSVVNVTAARKFQQEHQKQRE RDREQLKERTNSTQG VIR cDNA

681 QLSSCLSEAETAS CILSPASSLSASEAPDTPDPHSNTSPP AA Genomic
658 QLSSCLSEAETAS CILSPASSLSASEAPDTPDPHSNTSPP cDNA

721 PSLHTRPSVLHRTL TSTLR AA Genomic
698 PSLHTRPSVLHRTL TSTLR cDNA

FIGURE 4



Replacement Sheet

1 ATGGCAGCACGAGACGGGCAACACGGGCTCCACAGGATCCGCTGGCTCGACAGGATCGGGATCGGGATCGGGAAGTGGGAGC A
1 CAGCAGACGCGGGCAACACGGGCAACACAGGATCAGCTGGGTCCACA-----GGATCGGGATCGGGAACTGGGACG B
91 TCCTCAGATCCAGCGAATGGACGGGAGGCCCGTAACCTTGCCGAAAAACAGCGACGGGATAAGCTTAATGCCAGCATCCAGGAGCT A
72 TCCGCAGATCCAGCGAATGGACGGGAGGCCCGCAATCTTGCCGAGAAACAGCGACGGGATAAGCTTAATGCCAGCATCCAGGAGCT B
181 GGCTACCATGGTACCACATG-CAGCCGAATCCTCCCGTCGCCCTGGACAAACCGCCGTCCTTAGATTGCGCCACCC A
158 GGCTACCATGGTACCACATGTCAGCCGAATCCTCCCGACGCCCTGGACAAACCGCCGTCCTCAGATTGCGCCACCC B

FIGURE 5



Replacement Sheet

Fig. 6A

1
1 M A A T T A M P E M T S D V P S L G P A I A S G N S G P
1 M A D Q R M D I S S T I S D F
1 M A A P E . T G N T G S T G S A G S T G . S G S
1
L P D K L R
34 T E - L S D M V P T C S A L A R K P D K L T I L R M A V
110 T E - L S D M V P T C S A L A R K P D K L T I L R M A V
93 D E - L A S L V P T C N A M S R K L D K L T V L R M A V
67 Q E - L A T M V P H A A E S S R R L D K T A V L R F A T
47 L D R L A S L L P F P Q D V I N K L D K L S V L R L S V
H D Q L
120 S D W Y G T S L Y E H I H P D D R E K I R E Q L
202 S E W F G S T L Y D Q V H P D D V D K L R E Q L
106 N D L I G Q S L F D Y L H P K D I A K V K E Q L
102 S D L Y G Q N L L Q I T H P D D Q D L L R Q Q L I P R D
161 S D V I H Q S V Y E L I H T E D R A E F Q R Q L
R . F
104 - - R R G F I C . M R V G . - N V N P E S M V S G H L N
260 - - R R S F I C R M R C G S S S V D P V S V N R L S F V
244 - - R R S F F C R M K C N R P S V K V E D K D F P S T C
272 M D W R C F T V R L A R A S T R A E A T R H Y E R V K I
218 - - - R C F I C R L R C
H
270 T A - A N D M S G S N N Q S E F I T R H
348 S P N C T D M S N V C Q P T E F I S R H
325 V P Q P V N G E I R V K S M E Y V S R H
381 P P E E Y E G T V G C T I V N O P E P Y O L E Y N T R H
277 I L E I R T K N F I F R T K H

Match Line to Fig. 6B

Match Line to Fig. 6E



Replacement Sheet

Fig. 6B

Match Line to Fig. 6A

Match Line to Fig. 6C

Match Line to Fig. 6F

PAS B

D T E

AMDGKFTFVDQRVLNILGYTPTELLGK - I
NIEGIFTFVDHRCVATVGYQPQELLGK - N
AIDGKFVFVDQRAAILAYLPQELLGT - S
LIDGSIIDCDQRIGLVAGYNKOEVRNL - S
KLDFTPIIGCDAGRIVLGYTEAEELCTRGS

GIQGGGAIVQRAIKRRPGLDFDDDGEGNS
MSPGPTDLSSSLGTSGVDCNRKRKGSST
GSGSGSGSSSDPANG

AHMKALRGTGNTSDGTYKPSFLTDQ - - -
SHMKSLRGTGNTSTDGSYKPSFLTDQ - - -
QHMRTLRGATNPYTEANYKPTFLSDD - - -
HGLRLQYVFGKSASRRRKKPGLKOTGMSA
SYLRAKSFFDVALKSSPTERN - - GGQDNC
S

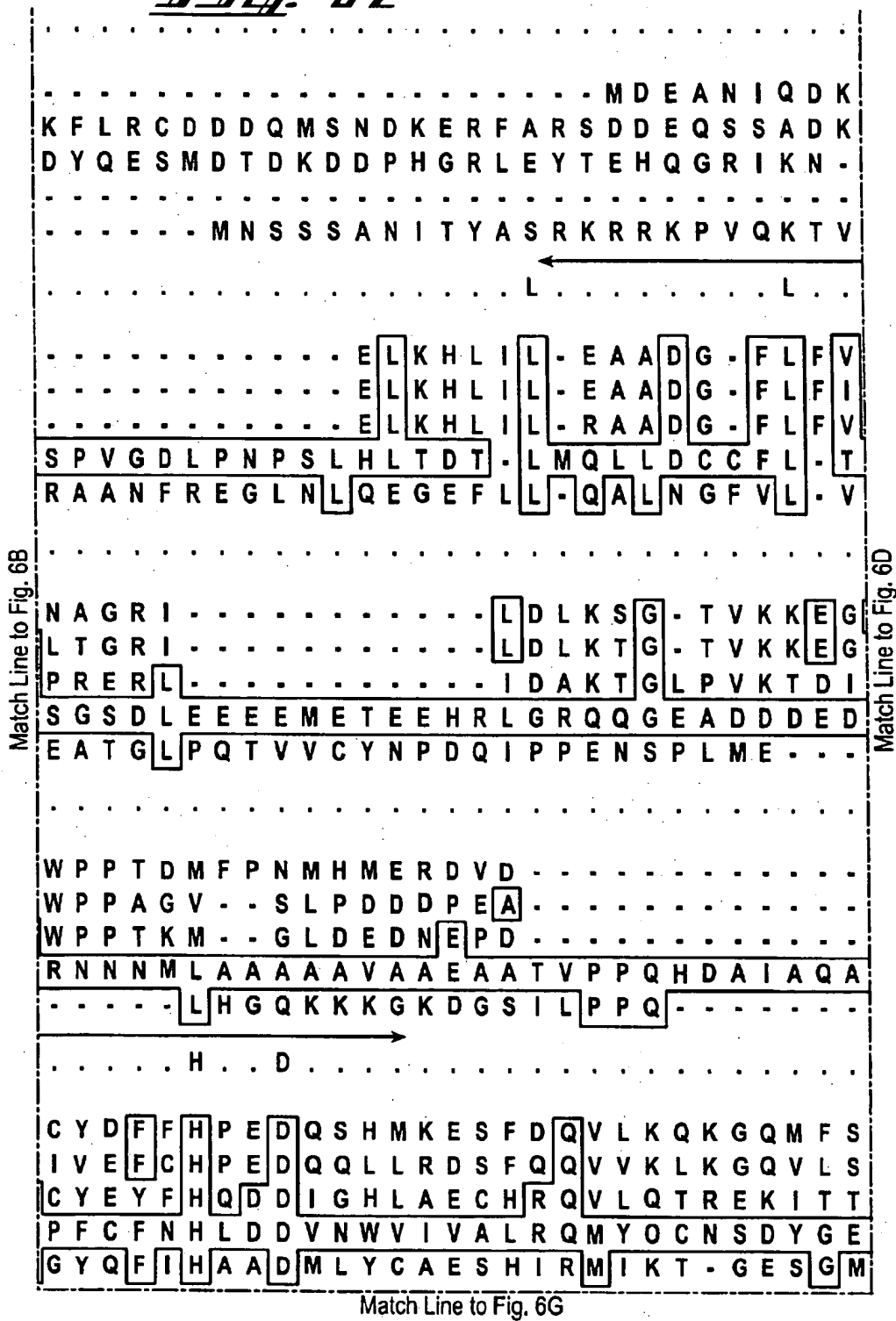
STQESQ
STSENA
SSSDTA
IETLFYQHQQHQQGHNPQQHSTSTSASAS
- HWALNPSQCTESGQGIE

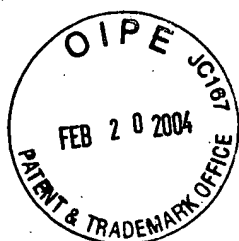
RLKQRNSLGP SRDG - TNYAVVHCTGYIKN
RNRCLRNGLGSVKDGEPHFVVHCTGYIKA
SKK KADRKSFCTTHSTGYLKS
DGCFRRSDDS SLTGGAAANYPIVVSQCIRRS
- LLDNSSGFLAMNFQGKLKY



Replacement Sheet

Fig. 6C





Replacement Sheet

Fig. 6D

.....	Consensus
ERFASRENHCEIERRRRNKMTAYI	Darnt
ERLA-RENHSEIERRRRNKMTAYI	Harnt
- - - - AREAHSQIEKR RRD KMNSFI	Bmal1
- - - - REARNLAEKQR RDKLNASI	Met_Orf
KPIPA-EGIKSNPSKRHRDRLNTE	Ahr_Human
PAS A	
..... S . S L . . . Q	Consensus #1
VSCDSGRVIVVSDSVTPV-LNYTQ	Darnt
VSCETGRVVVSDSVTPV-LNQPPQ	Harnt
VGCDRGKILFVSESVFKI-LNYSQ	Bmal1
LTC-SGQIVLVSTSV EQ L-LGHCQ	Met_Orf
VITTD-ALVFYAS-STIQDYLG FQQ	Ahr_Human
.....	Consensus #1
H QSSMR L SMGA	Darnt
Q QSSMR M CMGS	Harnt
T PGPSR L CSGA	Bmal1
HPYNRRTPSPRRMAHLATIDDR LR	Met_Orf
.....	Ahr_Human
..... L . A L	Consensus #1
- - - DMSSH-CCLV AIG-R-LQVTS	Darnt
- - - GQGSK-FCLV AIG-R-LQVTS	Harnt
- - - NEGCLNLSCLV AIG-R-LHSHV	Bmal1
ALHGISGNDIVLVAMA-RVLR EER	Met_Orf
- - - - - LALFMIA TP-LQPPS	Ahr_Human
.....	Consensus
LLYRARAKNSEYYVWLRTQAY AFL	Darnt
VMFRFRSKNQE-WLWMRTSSSFTFQ	Harnt
NCYKFKIKDGS-FITLRSRWF S FM	Bmal1
SCYRLLSRNGR-FIYLNTKOFLEV	Met_Orf
IVFRLLTKNNRW TWVQSNARLLYK	Ahr_Human

Match Line to Fig. 6H



Replacement Sheet

Match Line to Fig. 6A

370 N P Y T D E **V** E Y I V **C** T **N** S S G K
448 N P Y **S** D E I E Y I I **C** T **N** T N V K N S S Q E P R P T L
425 N P W T K E **V** E Y I V S T **N** T V V
489 **D** R G S N K V H S F L C V N T L L . **D** E E A G R Q . - **K**
477 N . . . G R P D Y I I V T Q R P L **T** **D** E E G T E H L R **K**

463 A P T P Q Q Q Q Q Q Q R P G **S** A Q T **T** P V
558 R F S E I Y H N I N A **D** Q S K G I S S S T V P A T Q Q L
500 A E E I M E I H R I R G S S P **S** S
673 **M** E S L M D D G Y S S P A N T L T L E E
477 S T A P F E N N F F N E S M N E C R **N** W Q D N T A P M G

636 T S P A R S **P** S G P **T** Y T Q
668 G V G S F Q T P **S** S F S **S** M S L P G A P T A **S** P G A A A
593 P S N D E A **A** M A V I M **S** L L E A D A G L G G P V D F S
870 **S** C I L S P A S S L S A S E A P D T P D P H S N T S P P
587 D S L S K S P F I P **S** D Y Q Q Q Q S L A L N **S** S C M V Q

621 A A D V G S H A D H V
700 L G D Q S N S Y N N E E F P D L T M F P P F S E
620
716
696 Y T Q N F I S C N Q P V L P Q H S K C T E L D Y P M G S

631
789
626
718
906 V K F

Consensus *Consensus #1*: When all match the residue of Met_Orf show the residue of Met_Orf, otherwise show **

Fig. 6E

Match Line to Fig. 6F

Replacement Sheet

Match Line to Fig. 6B

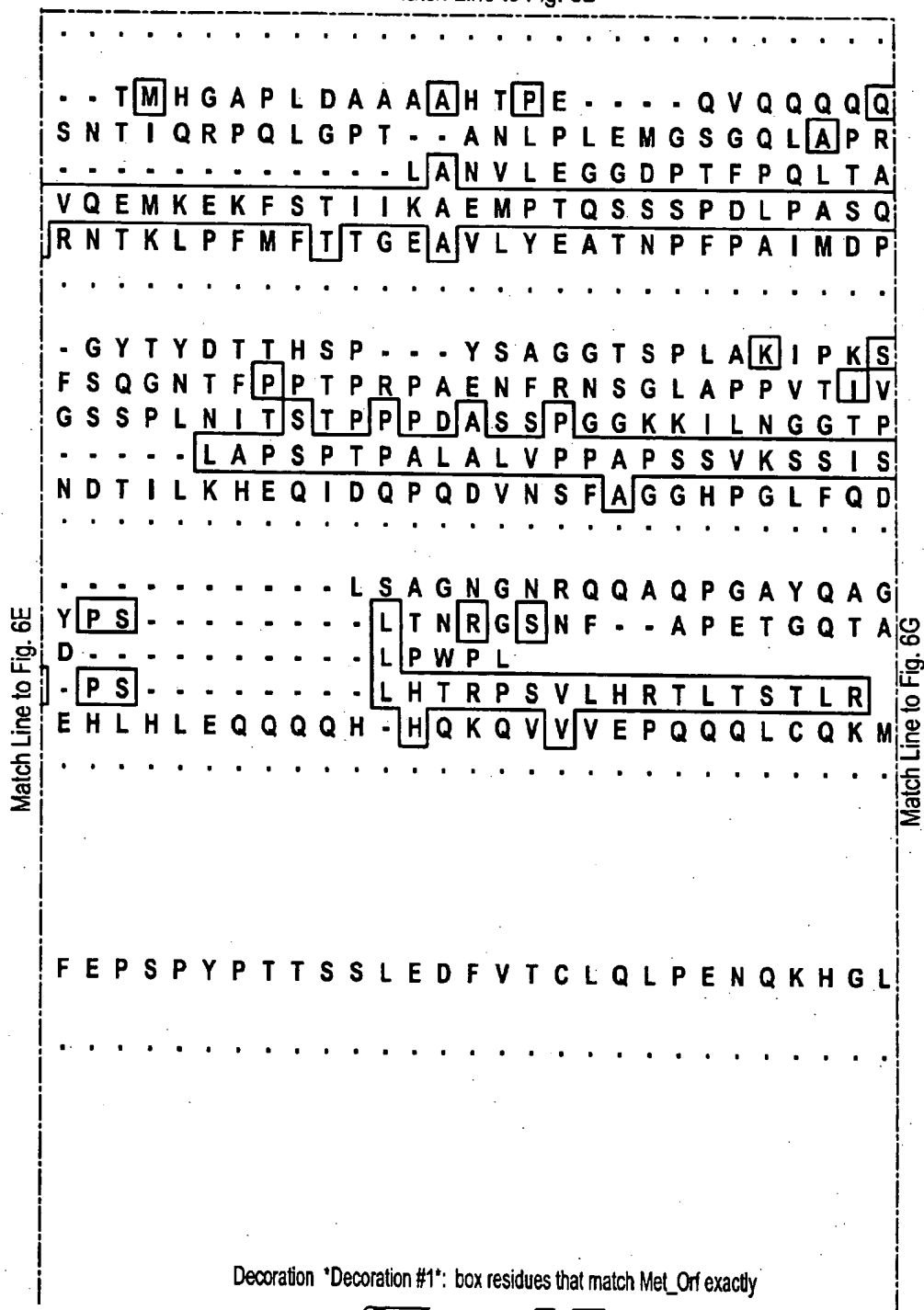


Fig. 6F



Replacement Sheet

Match Line to Fig. 6C

.....

Q Q Q E Q H V Y V Q A A P G V D - Y A R R E L T P V G S A
Q Q Q Q Q T E L D M V P G R D G L A S Y N H S Q V V Q P V
S P H S M D S M L P S G E G G P K R T H P T V P G I P G G
A P Q Q L E R I V L Y L I E N L Q K S V D S A E T V G G Q
L P L R T K N . . . G T S G K D S A T T S T L S K D S L N
.....

G T S P T P V A P N S
Q P S A S A G Q M L A Q I S R H S N P T Q G A T P T W T P
D I P S S G L L S G Q A Q E N P G Y P Y S D
K S V S V V N V T A A R K F Q Q E H Q K Q R E R D R E Q L
S K N S D L Y S I M K N L G I D F E D I R H M Q N E K F F
.....

P P P P P N A P G M W D W Q Q A G G H P H P P H P T A H P
G Q F Q T R T A E G V G V W P Q W Q G Q Q P H H R S S S S
.....

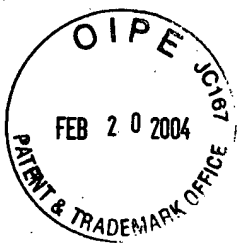
K H M Q V N G M F E N W N S N Q F V P F N C P Q Q D P Q Q
.....

N P Q S A I I T P Q T C Y A G A V S M Y Q C Q P E P Q H T
.....

Match Line to Fig. 6F

Match Line to Fig. 6H

Fig. 6G



Replacement Sheet

Match Line to Fig. 6D

Match Line to Fig. 6G

.....	Consensus
T N D G M Y Q T H M L A M Q	Darnt
T T T G P E H S K P L E K S D G L F A Q D R D P	Harnt
T R A G A G K I G R M I	Bmal 1
G	Met_Orf
P S S L L A A M M Q Q D E S I Y L Y P A S S T S	Ahr_Human
.....	Consensus
W A A L R P Q Q Q Q Q Q P V T E G Y Q Y Q Q	Darnt
T T R S G F S A Q Q V A T Q A T A K T R T S Q F	Harnt
S S S I L G E N P H I G I D M I D N D Q G S S S	Bmal 1
K E R T N S T Q G V I R Q L S S C L S E A E T A	Met_Orf
R N D F S G E V D F R D I D L T D E I L T Y V Q	Ahr_Human
.....	Consensus
H H P H A H P G G P A G A G Q P Q G Q G V L R Y	Darnt
E Q H V Q Q P P A Q Q P G Q P E V F Q E M L S M	Harnt
	Bmal 1
	Met_Orf
Y N V F T D L H G I S Q E F P Y K S E M D S M P	Ahr_Human
.....	Consensus
	Darnt
	Harnt
	Bmal 1
	Met_Orf
H V G Q M Q Y N P V L P G Q Q A F L N K F Q N G	Ahr_Human
.....	Consensus
	Darnt
	Harnt
	Bmal 1
	Met_Orf
	Ahr_Human

Fig. 6H



Replacement Sheet

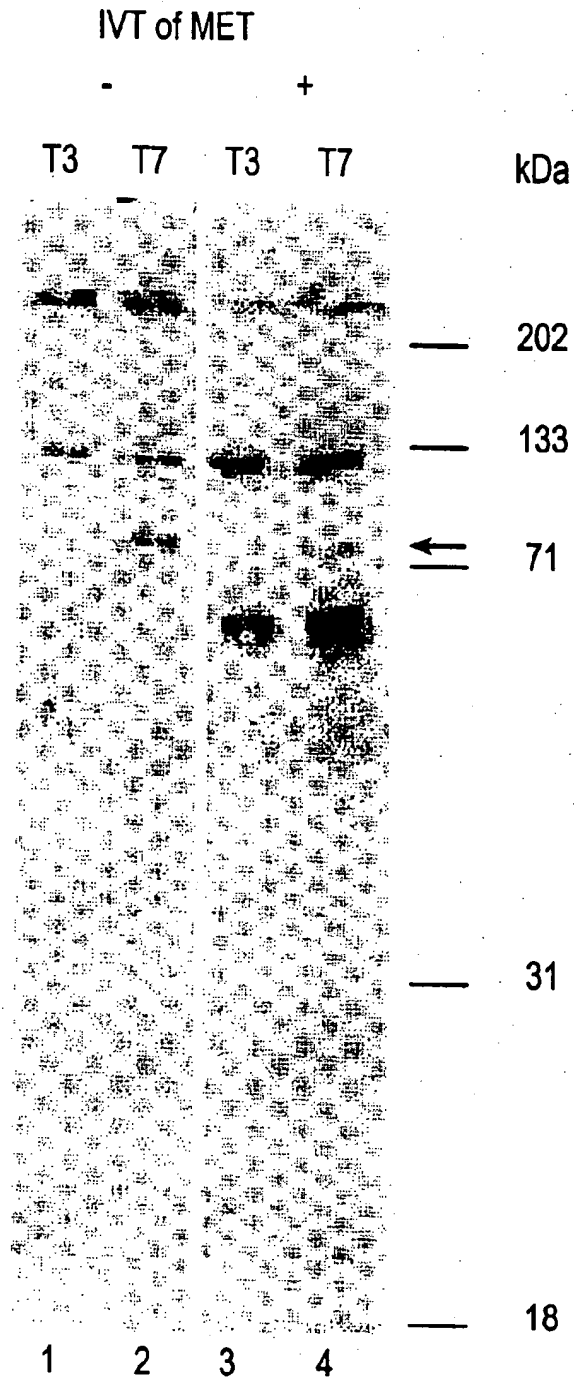


Fig. 1



Replacement Sheet

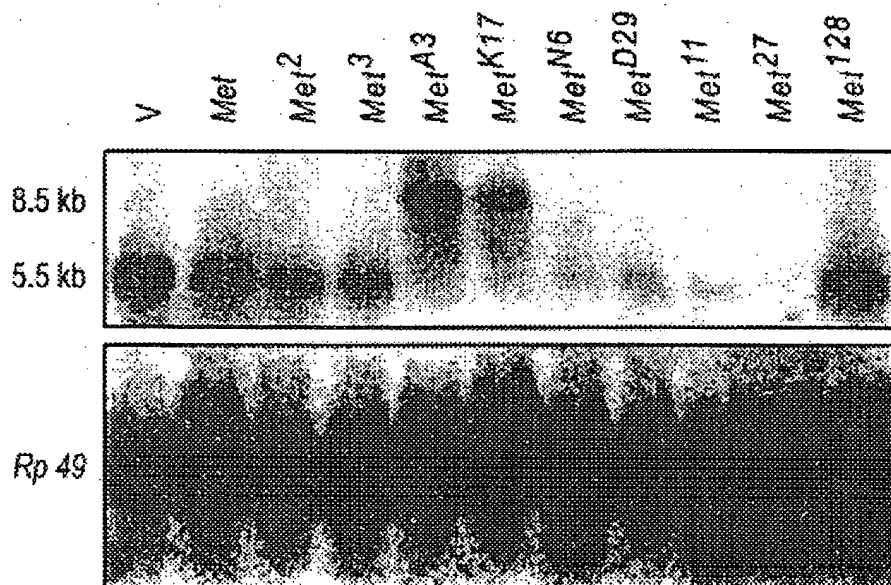


Fig. 8

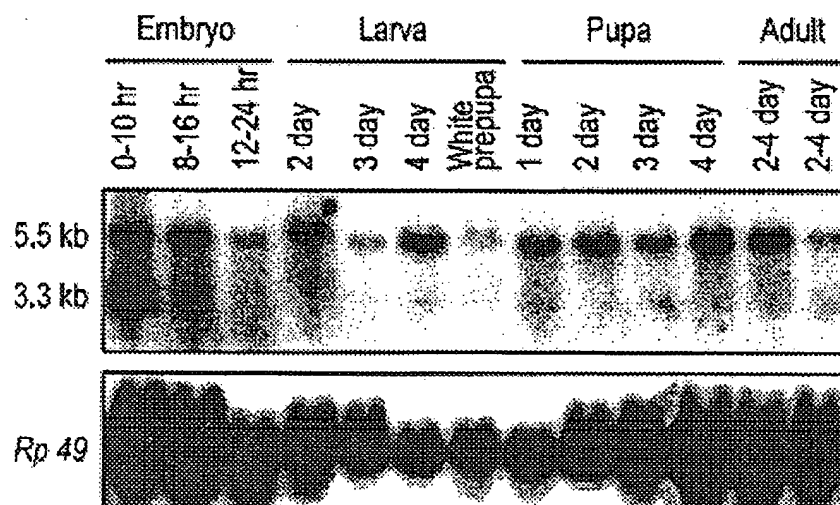


Fig. 9